

SEQUENCE LISTING

<110> Munger, Karl and Syken, Josh

<120> Methods and Reagents to Regulate Apoptosis

<130> HMV-054.01

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 2656

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (32)..(1474)

<400> 1

gaattcgcgg cccgagtc cccggggccaa g atg gct gcg cgg tgc tcc aca 52
Met Ala Ala Arg Cys Ser Thr
1 5

cgc tgg ttg ctg gtg gtt gtg ggg acc ccg cgg ctg ccg gct ata tcg 100
Arg Trp Leu Leu Val Val Gly Thr Pro Arg Leu Pro Ala Ile Ser
10 15

ggt aga ggg gcc ccg ccc agg gag ggc gtg gtg ggg gca tgg ctg 148
Gly Arg Gly Ala Arg Pro Pro Arg Glu Gly Val Val Gly Ala Trp Leu
25 30 35

agc cgc aag ctg agc gtc ccc gcc ttt gcg tct tcc ctg acc tct tgc 196
Ser Arg Lys Leu Ser Val Pro Ala Phe Ala Ser Ser Leu Thr Ser Cys
40 45 50 55

ggc ccc cga gcg ctg ctg aca ttg aga cct ggt gtc agc ctt aca gga 244
Gly Pro Arg Ala Leu Leu Thr Leu Arg Pro Gly Val Ser Leu Thr Gly
60 65 70

aca aaa cat aac cct ttc att tgt act gcc tcc ttc cac acg agt gcc 292
Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser Phe His Thr Ser Ala
75 80 85

cct ttg gcc aaa gaa gat tat tat cag ata tta gga gtg cct cga aat 340
Pro Leu Ala Lys Glu Asp Tyr Tyr Gln Ile Leu Gly Val Pro Arg Asn
90 95 100

gcc agc cag aaa gag atc aag aaa gcc tat tat cag ctt gcc aag aag 388
Ala Ser Gln Lys Glu Ile Lys Lys Ala Tyr Tyr Gln Leu Ala Lys Lys
105 110 115

tat cac cct gac aca aat aag gat gat ccc aaa gcc aag gag aag ttc 436
Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Lys Ala Lys Glu Lys Phe
120 125 130 135

tcc cag ctg gca gaa gcc tat gag gtt ttg agt gat gag gtg aag agg 484
Ser Gln Leu Ala Glu Ala Tyr Glu Val Leu Ser Asp Glu Val Lys Arg

FOLATE CYCLOPS

140	145	150	
aag cag tac gat gcc tac ggc tct gca ggc ttc gat cct ggg gcc agc Lys Gln Tyr Asp Ala Tyr Gly Ser Ala Gly Phe Asp Pro Gly Ala Ser 155	160	165	532
ggc tcc cag cat agc tac tgg aag gga ggc ccc act gtg gac ccc gag Gly Ser Gln His Ser Tyr Trp Lys Gly Gly Pro Thr Val Asp Pro Glu 170	175	180	580
gag ctg ttc agg aag atc ttt ggc gag ttc tca tcc tct tca ttt gga Glu Leu Phe Arg Lys Ile Phe Gly Glu Phe Ser Ser Ser Phe Gly 185	190	195	628
gat ttc cag acc gtg ttt gat cag cct cag gaa tac ttc atg gag ttg Asp Phe Gln Thr Val Phe Asp Gln Pro Gln Glu Tyr Phe Met Glu Leu 200	205	210	676
aca ttc aat caa gct gca aag ggg gtc aac aag gag ttc acc gtg aac Thr Phe Asn Gln Ala Ala Lys Gly Val Asn Lys Glu Phe Thr Val Asn 220	225	230	724
atc atg gac acg tgt gag cgc tgc aac ggc aag ggg aac gag ccc ggc Ile Met Asp Thr Cys Glu Arg Cys Asn Gly Lys Gly Asn Glu Pro Gly 235	240	245	772
acc aag gtg cag cat tgc cac tac tgt ggc ggc tcc ggc atg gaa acc Thr Lys Val Gln His Cys His Tyr Cys Gly Ser Gly Met Glu Thr 250	255	260	820
atc aac aca ggc cct ttt gtg atg cgt tcc acg tgt agg aga tgt ggt Ile Asn Thr Gly Pro Phe Val Met Arg Ser Thr Cys Arg Arg Cys Gly 265	270	275	868
ggc cgc ggc tcc atc atc ata tcg ccc tgt gtg gtc tgc agg gga gca Gly Arg Gly Ser Ile Ile Ser Pro Cys Val Val Cys Arg Gly Ala 280	285	290	916
gga caa gcc aag cag aaa aag cga gtg atg atc cct gtg cct gca gga Gly Gln Ala Lys Gln Lys Lys Arg Val Met Ile Pro Val Pro Ala Gly 300	305	310	964
gtc gag gat ggc cag acc gtg agg atg cct gtg gga aaa agg gaa att Val Glu Asp Gly Gln Thr Val Arg Met Pro Val Gly Lys Arg Glu Ile 315	320	325	1012
ttc att acg ttc agg gtg cag aaa agc cct gtg ttc cgg agg gac ggc Phe Ile Thr Phe Arg Val Gln Lys Ser Pro Val Phe Arg Arg Asp Gly 330	335	340	1060
gca gac atc cac tcc gac ctc ttt att tct ata gct cag gct ctt ctt Ala Asp Ile His Ser Asp Leu Phe Ile Ser Ile Ala Gln Ala Leu Leu 345	350	355	1108
ggg gga aca gcc aga ggc cag ggc ctg tac gag acg atc aac gtg acg Gly Gly Thr Ala Arg Ala Gln Gly Leu Tyr Glu Thr Ile Asn Val Thr 360	365	370	1156

atc ccc cct ggg act cag aca gac cag aag att cg ^g atg ggt ggg aaa Ile Pro Pro Gly Thr Gln Thr Asp Gln Lys Ile Arg Met Gly Gly Lys 380 385 390	1204
ggc atc ccc cg ^g att aac agc tac ggc tac gga gac cac tac atc cac Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr Gly Asp His Tyr Ile His 395 400 405	1252
atc aag ata cga gtt cca aag agg cta acg agc cg ^g cag cag agc ctg Ile Lys Ile Arg Val Pro Lys Arg Leu Thr Ser Arg Gln Gln Ser Leu 410 415 420	1300
atc ctg agc tac gcc gag gac gag aca gat gtg gag ggg acg gtg aac Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp Val Glu Gly Thr Val Asn 425 430 435	1348
ggc gtc acc ctc acc agc tct ggt ggc agc acc atg gat agc tcc gca Gly Val Thr Leu Thr Ser Ser Gly Ser Thr Met Asp Ser Ser Ala 440 445 450 455	1396
gga agc aag gct agg cgt gag gct ggg gag gac gag gag gga ttc ctt Gly Ser Lys Ala Arg Arg Glu Ala Gly Glu Asp Glu Glu Gly Phe Leu 460 465 470	1444
tcc aaa ctt aag aaa atg ttt acc tca tga tatcccagcc gagaaaaaaag Ser Lys Leu Lys Lys Met Phe Thr Ser 475 480	1494
atccactgga aactaggccg ggaaggcagca gcccctccaa gggccaggc acctgggaga	1554
cgggaggatt ccagaacagc agcaactgagc tcccacccgc agagcctctg gacggccttg	1614
gcaacagcaa aatcatggga caacacctct ctccacggaa aggtcacagt ggacagcccg	1674
ggcagtagga tgcagcccc gaggctggtg gcagtttctt gtccatttgtt aggtgacggc	1734
cccctggtca gcagaggaga gtttagatct tgcaggctaa aactctaatt tggaattgaa	1794
tattgtggat atcttagtta aaggccatgc ttacagctta gaaatgaagc cttaagctgc	1854
atcaagttac gaagtgatta atttccttct cagcaaacct ccgggaggtt ccagaatgag	1914
ttcttcctga cagttgtct tcactggag cgtggggccc ccaggcccc ccagcaccgt	1974
cctccccctaa tgaggggccc tgccgaggca tcagctgctc tgctcagttt gtttttattc	2034
ccggggtacc aagcagctgc acagtcggtg cctgggaagc acgttaaagg cccagagaga	2094
tcctgggggt tctgctctga ccgtgtgggt ggtgatcctt gtcaggatgt acagtccttg	2154
ctccccacccc atccggatg gccgcctgtc cctgactatt gagtcctgtt gttgtaagcc	2214
aggcatggag ggctcctgcc cttctgctga gcccacagccc attgcagcac tgtgctggcc	2274
agacttcagc tgccttggga actgaagccc tgccactgtt gctagtcagg ggcttggttc	2334

tcccaacttac actgttgaca tctatTTCT gaagtgtgtt taaatttttc agtgctaatc 2394
 attgtttttt cctttgtaaa tgTTGATTCA gaaaaggaaa gcacaggcta agcagttgaa 2454
 ggTTCCCAc cattcagtga gagcagaacc cccattcccc agcctctgct ggttagcatgt 2514
 cgCAGTTCC atgtgtttca ggatcttcgg gctgtcgta gacaggtaa tgaagaacac 2574
 ttctcaacag tttcTTTTT gTTTcCTTt ataattcact aaaataaagc atctattagt 2634
 gtctgaaaaa aaaaaaaaaa aa 2656

<210> 12
 <211> 480
 <212> PRT
 <213> homo sapiens
 <400> 2

Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
 1 5 10 15

Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
 20 25 30

Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
 35 40 45

Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
 50 55 60

Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
 65 70 75 80

Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
 85 90 95

Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
 100 105 110

Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
 115 120 125

Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
 130 135 140

Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
 145 150 155 160

Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
165 170 175

Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
180 185 190

Phe Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
195 200 205

Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
210 215 220

Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
225 230 235 240

Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
245 250 255

Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
260 265 270

Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
275 280 285

Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
290 295 300

Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
305 310 315 320

Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser
325 330 335

Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
340 345 350

Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
355 360 365

Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
370 375 380

Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
385 390 395 400

Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
405 410 415

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430

Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly
435 440 445

Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly
450 455 460

Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG GCT GCG CGG TGC TCC ACA CGC TGG TTG CTG GTG GTT GTG GGG ACC	48
Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr	
1 5 10 15	
CCG CGG CTG CCG GCT ATA TCG GGT AGA GGG GCC CGG CCG CCC AGG GAG	96
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu	
20 25 30	
GGC GTG GTG GGG GCA TGG CTG AGC CGC AAG CTG AGC GTC CCC GCC TTT	144
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe	
35 40 45	
GCG TCT TCC CTG ACC TCT TGC GGC CCC CGA GCG CTG CTG ACA TTG AGA	192
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg	
50 55 60	
CCT GGT GTC AGC CTT ACA GGA ACA AAA CAT AAC CCT TTC ATT TGT ACT	240
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr	
65 70 75 80	
GCC TCC TTC CAC ACG AGT GCC CCT TTG GCC AAA GAA GAT TAT TAT CAG	288
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln	
85 90 95	
ATA TTA GGA GTG CCT CGA AAT GCC AGC CAG AAA GAG ATC AAG AAA GCC	336
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala	
100 105 110	
TAT TAT CAG CTT GCC AAG AAG TAT CAC CCT GAC ACA AAT AAG GAT GAT	384

四庫全書

Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	
							115		120			125				432
CCC	AAA	GCC	AAG	GAG	AAG	TTC	TCC	CAG	CTG	GCA	GAA	GCC	TAT	GAG	GTT	
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val	
							130		135			140				480
TTG	AGT	GAT	GAG	GTG	AAG	AGG	AAG	CAG	TAC	GAT	GCC	TAC	GGC	TCT	GCA	
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala	
							145		150			155			160	528
GGC	TTC	GAT	CCT	GGG	GCC	AGC	GGC	TCC	CAG	CAT	AGC	TAC	TGG	AAG	GGA	
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	
							165		170			175				576
GGC	CCC	ACT	GTG	GAC	CCC	GAG	GAG	CTG	TTC	AGG	AAG	ATC	TTT	GGC	GAG	
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	
							180		185			190				624
TTC	TCA	TCC	TCT	TCA	TTT	GGA	GAT	TTC	CAG	ACC	GTG	TTT	GAT	CAG	CCT	
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	
							195		200			205				672
CAG	GAA	TAC	TTC	ATG	GAG	TTG	ACA	TTC	AAT	CAA	GCT	GCA	AAG	GGG	GTC	
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val	
							210		215			220				720
AAC	AAG	GAG	TTC	ACC	GTG	AAC	ATC	ATG	GAC	ACG	TGT	GAG	CGC	TGC	AAC	
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	
							225		230			235			240	768
GGC	AAG	GGG	AAC	GAG	CCC	GGC	ACC	AAG	GTG	CAG	CAT	TGC	CAC	TAC	TGT	
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	
							245		250			255				816
GGC	GGC	TCC	GGC	ATG	GAA	ACC	ATC	AAC	ACA	GGC	CCT	TTT	GTG	ATG	CGT	
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg	
							260		265			270				864
TCC	ACG	TGT	AGG	AGA	TGT	GGT	GGC	CGC	GGC	TCC	ATC	ATC	ATA	TCG	CCC	
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro	
							275		280			285				912
TGT	GTG	GTC	TGC	AGG	GGG	GCA	GGG	CAA	GCC	AAG	CAG	AAA	AAG	CGA	GTG	
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	
							290		295			300				960
ATG	ATC	CCT	GTG	CCT	GCA	GGA	GTC	GAG	GAT	GGC	CAG	ACC	GTG	AGG	ATG	
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	
							305		310			315			320	1008
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC	
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	
							325		330			335				1056
CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT	
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	
							340		345			350				1104
TCT	ATA	GCT	CAG	GCT	CTT	CTT	GGG	GGA	ACA	GCC	AGA	GCC	CAG	GGC	CTG	
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu	
							355		360			365				1152
TAC	GAG	ACG	ATC	AAC	GTG	ACG	ATC	CCC	CCT	GGG	ACT	CAG	ACA	GAC	CAG	
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	
							370		375			380				1200
AAG	ATT	CGG	ATG	GGT	GGG	AAA	GGC	ATC	CCC	CGG	ATT	AAC	AGC	TAC	GGC	
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	
							385		390			395			400	1248
TAC	GGA	GAC	CAC	TAC	ATC	CAC	ATC	AAG	ATA	CGA	GTT	CCA	AAG	AGG	CTA	
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu	
							405		410			415				1296
ACG	AGC	CGG	CAG	CAG	AGC	CTG	ATC	CTG	AGC	TAC	GCC	GAG	GAC	GAG	ACA	

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr			
420	425	430	
GAT GTG GAG GGG ACG GTG AAC GGC GTC ACC CTC ACC AGC TCT GGT GGC			1344
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly			
435	440	445	
AGC ACC ATG GAT AGC TCC GCA GGA AGC AAG GCT AGG CGT GAG GCT GGG			1392
Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly			
450	455	460	
GAG GAC GAG GAG GGA TTC CTT TCC AAA CTT AAG AAA ATG TTT ACC TCA			1440
Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser			
465	470	475	480
TGA			
		1443	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr			
1	5	10	15
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu			
20	25	30	
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe			
35	40	45	
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg			
50	55	60	
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr			
65	70	75	80
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln			
85	90	95	
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala			
100	105	110	
Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp			
115	120	125	
Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val			
130	135	140	
Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala			
145	150	155	160
Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly			
165	170	175	
Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu			
180	185	190	
Phe Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro			
195	200	205	
Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val			
210	215	220	
Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn			
225	230	235	240
Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys			
245	250	255	
Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg			
260	265	270	
Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro			
275	280	285	
Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val			

T0167206060

290	295	300
Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met		
305	310	315
Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser		320
325	330	335
Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile		
340	345	350
Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu		
355	360	365
Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln		
370	375	380
Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly		
385	390	395
Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu		400
405	410	415
Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr		
420	425	430
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly		
435	440	445
Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly		
450	455	460
Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser		
465	470	475
		480

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCT GCG CGG TGC TCC ACA CGC TGG TTG CTG GTG GTT GTG GGG ACC	48
Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr	
1 5 10 15	
CCG CGG CTG CCG GCT ATA TCG GGT AGA GGG GCC CGG CCG CCC AGG GAG	96
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu	
20 25 30	
GGC GTG GTG GGG GCA TGG CTG AGC CGC AAG CTG AGC GTC CCC GCC TTT	144
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe	
35 40 45	
GCG TCT TCC CTG ACC TCT TGC GGC CCC CGA GCG CTG CTG ACA TTG AGA	192
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg	
50 55 60	
CCT GGT GTC AGC CTT ACA GGA ACA AAA CAT AAC CCT TTC ATT TGT ACT	240
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr	
65 70 75 80	
GCC TCC TTC CAC ACG AGT GCC CCT TTG GCC AAA GAA GAT TAT TAT CAG	288
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln	
85 90 95	
ATA TTA GGA GTG CCT CGA AAT GCC AGC CAG AAA GAG ATC AAG AAA GCC	336
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala	
100 105 110	
TAT TAT CAG CTT GCC AAG AAG TAT CAC CCT GAC ACA AAT AAG GAT GAT	384

F05EYD0660

Tyr	Tyr	Gln	Leu	Ala	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	
115						120					125				
CCC	AAA	GCC	AAG	GAG	AAG	TTC	TCC	CAG	CTG	GCA	GAA	GCC	TAT	GAG	GTT
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val
130						135					140				
TTG	AGT	GAT	GAG	GTG	AAG	AGG	AAG	CAG	TAC	GAT	GCC	TAC	GGC	TCT	GCA
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala
145						150					155			160	
GGC	TTC	GAT	CCT	GGG	GCC	AGC	GGC	TCC	CAG	CAT	AGC	TAC	TGG	AAG	GGA
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly
165						170					175				
GGC	CCC	ACT	GTG	GAC	CCC	GAG	GAG	CTG	TTC	AGG	AAG	ATC	TTT	GGC	GAG
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu
180						185					190				
TTC	TCA	TCC	TCT	TCA	TTT	GGA	GAT	TTC	CAG	ACC	GTG	TTT	GAT	CAG	CCT
Phe	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	
195						200					205				
CAG	GAA	TAC	TTC	ATG	GAG	TTG	ACA	TTC	AAT	CAA	GCT	GCA	AAG	GGG	GTC
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val
210						215					220				
AAC	AAG	GAG	TTC	ACC	GTG	AAC	ATC	ATG	GAC	ACG	TGT	GAG	CGC	TGC	AAC
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn
225						230					235			240	
GGC	AAG	GGG	AAC	GAG	CCC	GGC	ACC	AAG	GTG	CAG	CAT	TGC	CAC	TAC	TGT
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys
245						250					255				
GGC	GGC	TCC	GGC	ATG	GAA	ACC	ATC	AAC	ACA	GGC	CCT	TTT	GTG	ATG	CGT
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg
260						265					270				
TCC	ACG	TGT	AGG	AGA	TGT	GGT	GGC	CGC	GGC	TCC	ATC	ATC	ATA	TCG	CCC
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro
275						280					285				
TGT	GTG	GTC	TGC	AGG	GGG	GCA	GGG	CAA	GCC	AAG	CAG	AAA	AAG	CGA	GTG
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val
290						295					300				
ATG	ATC	CCT	GTG	CCT	GCA	GGG	GTC	GAG	GAT	GGC	CAG	ACC	GTG	AGG	ATG
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met
305						310					315			320	
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser
325						330					335				
CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile
340						345					350				
TCT	ATA	GCT	GCT	CTT	CTT	GGG	GGG	ACA	GCA	GCC	CAG	GGC	CTG		
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu
355						360					365				
TAC	GAG	ACG	ATC	AAC	GTG	ACG	ATC	CCC	CCT	GGG	ACT	CAG	ACA	GAC	CAG
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln
370						375					380				
AAG	ATT	CGG	ATG	GGT	GGG	AAA	GGC	ATC	CCC	CGG	ATT	AAC	AGC	TAC	GGC
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly
385						390					395			400	
TAC	GGA	GAC	CAC	TAC	ATC	CAC	ATC	AAG	ATA	CGA	GTT	CCA	AAG	AGG	CTA
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu
405						410					415				
ACG	AGC	CGG	CAG	CAG	AGC	CTG	ATC	CTG	AGC	TAC	GCC	GAG	GAC	GAG	ACA

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr			
420	425	430	
GAT GTG GAG GGG ACG GTG AAC GGC GTC ACC CTC ACC AGC TCT GGA AAA			1344
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys			
435	440	445	
AGA TCC ACT GGA AAC TAG			1362
Arg Ser Thr Gly Asn			
450			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr			
1	5	10	15
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu			
20	25	30	
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe			
35	40	45	
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg			
50	55	60	
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr			
65	70	75	80
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln			
85	90	95	
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala			
100	105	110	
Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp			
115	120	125	
Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val			
130	135	140	
Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala			
145	150	155	160
Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly			
165	170	175	
Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu			
180	185	190	
Phe Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro			
195	200	205	
Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val			
210	215	220	
Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn			
225	230	235	240
Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys			
245	250	255	
Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg			
260	265	270	
Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro			
275	280	285	
Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val			
290	295	300	
Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met			
305	310	315	320
Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser			

325 330 335
Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
340 345 350
Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
355 360 365
Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
370 375 380
Lys Ile Arg Met Gly Gly Ile Pro Arg Ile Asn Ser Tyr Gly
385 390 395 400
Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
405 410 415
Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys
435 440 445
Arg Ser Thr Gly Asn
450

20256200660